SEQUENCE LISTING

- (1) GENERAL INFORMATION
- (i) APPLICANT: SEED, BRIAN HAAS, JURGEN
- (ii) TITLE OF THE INVENTION: HIGH LEVEL EXPRESSION OF PROTEINS
- (iii) NUMBER OF SEQUENCES: 110
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Clark & Elbing LLP
 - (B) STREET: 176 Federal Street
 - (C) CITY: Boston
 - (D) STATE: MA

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- (E) COUNTRY: USA
- (F) ZIP: 02110
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/717,294
 - (B) FILING DATE: 20-SEP-1996
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Elbing, Karen L
 - (B) REGISTRATION NUMBER: 35,238
 - (C) REFERENCE/DOCKET NUMBER: 00786/345001
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 617-428-0200
 - (B) TELEFAX: 617-428-7045
 - (C) TELEX:
 - (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Other
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGCGGGCTAG CCACCGAGAA GCTG

- (2) INFORMATION FOR SEQ ID NO:2:
- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 195 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Other	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:	
ACCGAGAAGC TGTGGGTGAC CGTGTACTAC GGCGTGCCCG TGTGGAAGAG AGGCCACCAC CACCCTGTTC TGCGCCAGCG ACGCCAAGGC GTACGACACC GAGGTGCACA ACGTGTGGGC CACCCAGGCG TGCGTGCCCA CCGACCCCAA CCCCCAGGAG GTGGAGCTCG TGAACGTGAC CGAGAACTTC AACAT	60 120 180 195
(2) INFORMATION FOR SEQ ID NO:3:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 34 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: Other	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:	
CCACCATGTT GTTCTTCCAC ATGTTGAAGT TCTC	34
(2) INFORMATION FOR SEQ ID NO:4:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 33 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Other	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:	
GACCGAGAAC TTCAACATGT GGAAGAACAA CAT	33
(2) INFORMATION FOR SEQ ID NO:5:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 192 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: Other	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:	
TGGAAGACA ACATGGTGGA GCAGATGCAT GAGGACATCA TCAGCCTGTG GGACCAGAGC CTGAAGCCCT GCGTGAAGCT GACCCCCTGT GCGTGACCTG AACTGCACCG ACCTGAGGAA CACCACCAAC ACCAACACAG CACCGCCAAC AACAACAGCA ACAGCGAGGG CACCATCAAG GGCGGCGAGA TG	60 120 180 192
(2) INFORMATION FOR SEQ ID NO:6:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 33 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single	

(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Other	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:	
GTTGAAGCTG CAGTTCTTCA TCTCGCCGCC CTT	33
(2) INFORMATION FOR SEQ ID NO:7:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 31 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: Other	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:	
GAAGAACTGC AGCTTCAACA TCACCACCAG C	31
(2) INFORMATION FOR SEQ ID NO:8:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 195 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: Other	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:	
AACATCACCA CCAGCATCCG CGACAAGATG CAGAAGGAGT ACGCCCTGCT GTACAAGCTG GATATCGTGA GCATCGACAA CGACAGCACC AGCTACCGCC TGATCTCCTG CAACACCAGC GTGATCACCC AGGCCTGCCC CAAGATCAGC TTCGAGCCCA TCCCCATCCA CTACTGCGCC CCCGCCGGCT TCGCC	60 120 180 195
(2) INFORMATION FOR SEQ ID NO:9:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: Other	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:	
GAACTTCTTG TCGGCGGCGA AGCCGGCGGG	3 0
(2) INFORMATION FOR SEQ ID NO:10:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 47 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: Other	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCGCCCCGC CGGCTTCGCC ATCCTGAAGT GCAACGACAA GAAGTTC	47
(2) INFORMATION FOR SEQ ID NO:11:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 198 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: Other	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:	
GCCGACAAGA AGTTCAGCGG CAAGGGCAGC TGCAAGAACG TGAGCACCGT GCAGTGCACC CACGGCATCC GGCCGGTGGT GAGCACCCAG CTCCTGCTGA ACGGCAGCCT GGCCGAGGAG GAGGTGGTGA TCCGCAGCGA GAACTTCACC GACAACGCCA AGACCATCAT CGTGCACCTG AATGAGAGCG TGCAGATC	60 120 180 198
(2) INFORMATION FOR SEQ ID NO:12:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 34 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: Other	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:	
AGTTGGGACG CGTGCAGTTG ATCTGCACGC TCTC	34
(2) INFORMATION FOR SEQ ID NO:13:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: Other	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:	
GAGAGCGTGC AGATCAACTG CACGCGTCCC	30
(2) INFORMATION FOR SEQ ID NO:14:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 120 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: Other	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:	
AACTGCACGC GTCCCAACTA CAACAAGCGC AAGCGCATCC ACATCGGCCC CGGGCGCGCC TTCTACACCA CCAAGAACAT CATCGGCACC ATCCTCCAGG CCCACTGCAA CATCTCTAGA	60 120
(2) INFORMATION FOR SEQ ID NO:15:	
(i) SEQUENCE CHARACTERISTICS:	

(A) LENGTH: 30 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Other
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
GTCGTTCCAC TTGGCTCTAG AGATGTTGCA 30
(2) INFORMATION FOR SEQ ID NO:16:
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 29 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Other
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
GCAACATCTC TAGAGCCAAG TGGAACGAC 29
(2) INFORMATION FOR SEQ ID NO:17:
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 131 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Other
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:
GCCAAGTGGA ACGACACCCT GCGCCAGATC GTGAGCAAGC TGAAGGAGCA GTTCAAGAAC AAGACCATCG TGTTCACCAG AGCAGCGGCG GCGACCCCGA GATCGTGATG CACAGCTTCA 120 ACTGCGGCGG C
(2) INFORMATION FOR SEQ ID NO:18:
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 29 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Other
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:
GCAGTAGAAG AATTCGCCGC CGCAGTTGA 29
(2) INFORMATION FOR SEQ ID NO:19:
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 29 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:	
TCAACTGCGG CGGCGAATTC TTCTACTGC	29
(2) INFORMATION FOR SEQ ID NO:20:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 195 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	•
(ii) MOLECULE TYPE: Other	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:	
GGCGAATTCT TCTACTGCAA CACCAGCCCC CTGTTCAACA GCACCTGGAA CGGCAACAAC ACCTGGAACA ACACCACCGG CAGCAACAAC AATATTACCC TCCAGTGCAA GATCAAGCAG ATCATCAACA TGTGGCAGGA GGTGGGCAAG GCCATGTACG CCCCCCCAT CGAGGGCCAG ATCCGGTGCA GCAGC	60 120 180 195
(2) INFORMATION FOR SEQ ID NO:21:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 40 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: Other	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:	
GCAGACCGGT GATGTTGCTG CTGCACCGGA TCTGGCCCTC	40
(2) INFORMATION FOR SEQ ID NO:22:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 40 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: Other	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:	
CGAGGGCCAG ATCCGGTGCA GCAGCAACAT CACCGGTCTG	40
(2) INFORMATION FOR SEQ ID NO:23:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 198 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: Other	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:	
AACATCACCG GTCTGCTGCT GACCCGCGAC GGCGGCAAGG ACACCGACAC CAACGACACC GAAATCTTCC GCCCCGGCGG CGGCGACATG CGCGACAACT GGAGATCTGA GCTGTACAAG TACAAGGTGG TGACGATCGA GCCCCTGGGC GTGGCCCCCA CCAAGGCCAA GCGCCGCGTG GTGCAGCGCG AGAAGCGC	60 120 180 198

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 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 38 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: Other	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:	
CGCGGGCGC CGCTTTAGCG CTTCTCGCGC TGCACCAC	38
(2) INFORMATION FOR SEQ ID NO:25:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: Other	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:	
CGCGGGGGAT CCAAGCTTAC CATGATTCCA GTAATAAGT	39
(2) INFORMATION FOR SEQ ID NO:26:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 165 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: Other	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:	
ATGAATCCAG TAATAAGTAT AACATTATTA TTAAGTGTAT TACAAATGAG TAGAGGACAA AGAGTAATAA GTTTAACAGC ATCTTTAGTA AATCAAAATT TGAGATTAGA TTGTAGACAT GAAAATAATA CAAATTTGCC AATACAACAT GAATTTTCAT TAACG	60 120 165
(2) INFORMATION FOR SEQ ID NO:27:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 36 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Other	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:	
CGCGGGGAAT TCACGCGTTA ATGAAAATTC ATGTTG	36
(2) INFORMATION FOR SEQ ID NO:28:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single 	

(2) INFORMATION FOR SEQ ID NO:24:

(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Other	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:	
CGCGGATCCA CGCGTGAAAA AAAAAAACAT	30
(2) INFORMATION FOR SEQ ID NO:29:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 150 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: Other	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:	
CGTGAAAAA AAAAACATGT ATTAAGTGGA ACATTAGGAG TACCAGAACA TACATATAGA AGTAGAGTAA ATTTGTTTAG TGATAGATTC ATAAAAGTAT TAACATTAGC AAATTTTACA ACAAAAGATG AAGGAGATTA TATGTGTGAG	60 120 150
(2) INFORMATION FOR SEQ ID NO:30:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: Other	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:	
CGCGAATTCG AGCTCACACA TATAATCTCC	30
(2) INFORMATION FOR SEQ ID NO:31:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: Other	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:	
CGCGGATCCG AGCTCAGAGT AAGTGGACAA	30
(2) INFORMATION FOR SEQ ID NO:32:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 170 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: Other	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:	
CTCAGAGTAA GTGGACAAAA TCCAACAAGT AGTAATAAAA CAATAAATGT AATAAGAGAT	60

AAATTAGTAA AATGTGAGGA ATAAGTTTAT TAGTACAAAA TACAAGTTGG TTATTATTAT TATTATTAAG TTTAAGTTTT TTACAAGCAA CAGATTTTAT AAGTTTATGA	120 170
(2) INFORMATION FOR SEQ ID NO:33:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 36 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(2.1) NOT BOTT B. ONL.	
(ii) MOLECULE TYPE: Other	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:	
CGCGAATTCG CGGCCGCTTC ATAAACTTAT AAAATC	36
(2) INFORMATION FOR SEQ ID NO:34:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 1632 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:	
CTCGAGATCC ATTGTGCTCT AAAGGAGATA CCCGGCCAGA CACCCTCACC TGCGGTGCCC	60
AGCTGCCCAG GCTGAGGCAA GAGAAGGCCA GAAACCATGC CCATGGGGTC TCTGCAACCG	120
CTGGCCACCT TGTACCTGCT GGGGATGCTG GTCGCTTCCG TGCTAGCCAC CGAGAAGCTG TGGGTGACCG TGTACTACGG CGTGCCCGTG TGGAAGGAGG CCACCACCAC CCTGTTCTGC	180
TGGGTGACCG TGTACTACGG CGTGCCCGTG TGGAAGGAGG CCACCACCAC CCTGTTCTGC GCCAGCGACG CCAAGGCGTA CGACACCGAG GTGCACAACG TGTGGGCCAC CCAGGCGTGC	240 300
GTGCCCACCG ACCCCAACCC CCAGGAGGTG GAGCTCGTGA ACGTGACCGA GAACTTCAAC	360
ATGTGGAAGA ACAACATGGT GGAGCAGATG CATGAGGACA TCATCAGCCT GTGGGACCAG	420
AGCCTGAAGC CCTGCGTGAA GCTGACCCCC CTGTGCGTGA CCCTGAACTG CACCGACCTG	480
AGGAACACCA CCAACACCAA CAACAGCACC GCCAACAACA ACAGCAACAG CGAGGGCACC	540
ATCAAGGGCG GCGAGATGAA CAACTGCAGC TTCAACATCA CCACCAGCAT CCGCGACAAG	600
ATGCAGAAGG AGTACGCCCT GCTGTACAAG CTGGATATCG TGAGCATCGA CAACGACAGC	660
ACCAGCTACC GCCTGATCTC CTGCAACACC AGCGTGATCA CCCAGGCCTG GCCCAAGATC	720
AGCTTCGAGC CCATCCCCAT CCACTACTGC GCCCCCGCCG GCTTCGCCAT CCTGAAGTGC	780

ATCGGCCCC GGCGCGCCTT CTACACCACC AAGAACATCA TCGGCACCAT CCGCCAGGCC 1080
CACTGCAACA TCTCTAGAGC CAAGTGGAAC GACACCCTGC GCCAGATCGT GAGCAAGCTG 1140
AAGGAGCAGT TCAAGAACAA GACCATCGTG TTCAACCAGA GCAGCGGCGG CGACCCCGAG 1200
ATCGTGATGC ACAGCTTCAA CTGCGGCGGC GAATTCTTCT ACTGCAACAC CAGCCCCCTG 1260
TTCAACAGCA CCTGGAACGG CAACAACACC TGGAACAACA CCACCGGCAG CAACAACAAT 1320
ATTACCCTCC AGTGCAAGAT CAAGCAGATC ATCAACATGT GGCAGGAGGT GGGCAAGGCC 1380
ATGTACGCCC CCCCCATCGA GGGCCAGATC CGGTGCAGCA GCAACATCAC CGGTCTGCTG 1440

840

900

960

1020

1500

1560

1620

1632

AACGACAAGA AGTTCAGCGG CAAGGGCAGC TGCAAGAACG TGAGCACCGT GCAGTGCACC

CACGGCATCC GGCCGGTGGT GAGCACCCAG CTCCTGCTGA ACGGCAGCCT GGCCGAGGAG

GAGGTGGTGA TCCGCAGCGA GAACTTCACC GACAACGCCA AGACCATCAT CGTGCACCTG

AATGAGAGCG TGCAGATCAA CTGCACGCGT CCCAACTACA ACAAGCGCAA GCGCATCCAC

CTGACCCGCG ACGGCGCAA GGACACCGAC ACCAACGACA CCGAAATCTT CCGCCCCGGC

GGCGGCGACA TGCGCGACAA CTGGAGATCT GAGCTGTACA AGTACAAGGT GGTGACGATC

GAGCCCCTGG GCGTGGCCCC CACCAAGGCC AAGCGCCGCG TGGTGCAGCG CGAGAAGCGC

- (2) INFORMATION FOR SEQ ID NO:35:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2481 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

TAAAGCGGCC GC

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

7 0007 07 7 00	попосополо	CCECETA CETA C	aaaamaaaaa	mamaan naan		C 0
ACCGAGAAGC				TGTGGAAGGA		60
ACCCTGTTCT	GCGCCAGCGA	CGCCAAGGCG	TACGACACCG	AGGTGCACAA	CGTGTGGGCC	120
ACCCAGGCGT	GCGTGCCCAC	CGACCCCAAC	CCCCAGGAGG	TGGAGCTCGT	GAACGTGACC	180
GAGAACTTCA	ACATGTGGAA	GAACAACATG	CTGGAGCAGA	TGCATGAGGA	CATCATCAGC	240
CTGTGGGACC	AGAGCCTGAA	GCCCTGCGTG	AAGCTGACCC	CCCTGTGCGT	GACCCTGAAC	300
TGCACCGACC	TGAGGAACAC	CACCAACACC	AACAACAGCA	CCGCCAACAA	CAACAGCAAC	360
AGCGAGGGCA	CCATCAAGGG	CGGCGAGATG	AAGAACTGCA	GCTTCAACAT	CACCACCAGC	420
ATCCGCGACA	AGATGCAGAA	GGAGTACGCC		AGCTGGATAT	CGTGAGCATC	480
CACAACGACA	GCACCAGCTA	CCGCCTGATC	TCCTGCAACA	CCAGCGTGAT	CACCCAGGCC	540
TGCCCCAAGA	TCAGCTTCGA	GCCCATCCCC	ATCCACTACT	GCGCCCCGC	CGGCTTCGCC	600
ATCCTGAAGT	GCAACGACAA	GAAGTTCAGC	GGCAAGGGCA	GCTGCAAGAA	CGTGACCACC	660
GTGCAGTGCA	CCCACGGCAT	CCGGCCGGTG	GTGAGCACCC	AGCTCCTGCT	GAACGGCAGC	720
CTGGCCGAGG	AGGAGGTGGT	GATCCGCAGC	GAGAACTTCA	CCGACAACGC	CAAGACCATC	780
ATCGTGCACC	TGAATGAGAG	CGTGCAGATC	AACTGCACGC	GTCCCAACTA	CAACAAGCGC	840
AAGCGCATCC	ACATCGGCCC	CGGGCGCCC	TTCTACACCA	CCAAGAACAT	CATCGGCACC	900
ATCCGCCAGG	CCCACTGCAA	CATCTCTAGA	GCCAAGTGGA	ACGACAÇCCT	GCGCCAGATC	960
GTGAGCAAGC	TGAAGGAGCA	GTTCAAGAAC	AAGACCATCG	TGTTCAÁCCA	GAGCAGCGGC	1020
GGCGACCCCG	AGATCGTGAT	GCACAGCTTC	AACTGCGGCG	GCGAATTCTT	CTACTGCAAC	1080
ACCAGCCCCC	TGTTCAACAG	CACCTGGAAC	GGCAACAACA	CCTGGAACAA	CACCACCGGC	1140
AGCAACAACA	ATATTACCCT	CCAGTGCAAG	ATCAAGCAGA	TCATCAACAT	GTGGCAGGAG	1200
GTGGGCAAGG	CCATGTACGC	CCCCCCATC	GAGGGCCAGA	TCCGGTGCAG	CAGCAACATC	1260
ACCGGTCTGC	TGCTGACCCG	CGACGGCGGC	AAGGACACCG	ACACCAACGA	CACCGAAATC	1320
TTCCGCCCCG	GCGGCGGCGA	CATGCGCGAC	AACTGGAGAT	CTGAGCTGTA	CAAGTACAAG	1380
GTGGTGACGA	TCGAGCCCCT	GGGCGTGGCC	CCCACCAAGG	CCAAGCGCCG	CGTGGTGCAG	1440
CGCGAGAAGC	GGGCCGCCAT	CGGCGCCCTG	TTCCTGGGCT	TCCTGGGGGC	GGCGGGCAGC	1500
ACCATGGGGG	CCGCCAGCGT	GACCCTGACC	GTGCAGGCCC	GCCTGCTCCT	GAGCGGCATC	1560
GTGCAGCAGC	AGAACAACCT	CCTCCGCGCC	ATCGAGGCCC	AGCAGCATAT	GCTCCAGCTC	1620
ACCGTGTGGG	GCATCAAGCA	GCTCCAGGCC	CGCGTGCTGG	CCGTGGAGCG	CTACCTGAAG	1680
GACCAGCAGC	TCCTGGGCTT	CTGGGGCTGC	TCCGGCAAGC	TGATCTGCAC	CACCACGGTA	1740
CCCTGGAACG	CCTCCTGGAG	CAACAAGAGC	CTGGACGACA	TCTGGAACAA	CATGACCTGG	1800
ATGCAGTGGG	AGCGCGAGAT	CGATAACTAC	ACCAGCCTGA	TCTACAGCCT	GCTGGAGAAG	1860
AGCCAGACCC	AGCAGGAGAA	GAACGAGCAG	GAGCTGCTGG	AGCTGGACAA	CTGGGCGAGC	1920
CTGTGGAACT	GGTTCGACAT	CACCAACTGG	CTGTGGTACA	TCAAAATCTT	CATCATGATT	1980
GTGGGCGGCC	TGGTGGGCCT	CCGCATCGTG	TTCGCCGTGC	TGAGCATCGT	GAACCGCGTG	2040
CGCCAGGGCT	ACAGCCCCCT	GAGCCTCCAG	ACCCGGCCCC	CCGTGCCGCG	CGGGCCCGAC	2100
CGCCCCGAGG	GCATCGAGGA	GGAGGGCGGC	GAGCGCGACC	GCGACACCAG	CGGCAGGCTC	2160
GTGCACGGCT	TCCTGGCGAT	CATCTGGGTC	GACCTCCGCA	GCCTGTTCCT	GTTCAGCTAC	2220
CACCACCGCG	ACCTGCTGCT	GATCGCCGCC	CGCATCGTGG	AACTCCTAGG	CCGCCGCGGC	2280
TGGGAGGTGC	TGAAGTACTG	GTGGAACCTC	CTCCAGTATT	GGAGCCAGGA	GCTGAAGTCC	2340
AGCGCCGTGA	GCCTGCTGAA	CGCCACCGCC	ATCGCCGTGG	CCGAGGGCAC	CGACCGCGTG	2400
ATCGAGGTGC	TCCAGAGGGC		ATCCTGCACA		CATCCGCCAG	2460
GGGCTCGAGA						2481
3220100	2223021001	-				2.01

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 486 base pairs (B) TYPE: nucleic acid

 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

ATGAATCCAG	TAATAAGTAT	AACATTATTA	TTAAGTGTAT	TACAAATGAG	TAGAGGACAA	60
AGAGTAATAA	GTTTAACAGC	ATGTTTAGTA	AATCAAAATT	TGAGATTAGA	TTGTAGACAT	120
GAAAATAATA	CACCTTTGCC	AATACAACAT	GAATTTTCAT	TAACGCGTGA	AAAAAAAAA	180
CATGTATTAA	GTGGAACATT	AGGAGTACCA	GAACATACAT	ATAGAAGTAG	AGTAAATTTG	240
TTTAGTGATA	GATTCATAAA	AGTATTAACA	TTAGCAAATT	TTACAACAAA	AGATGAAGGA	300

GATTATATGT GTGAGCTCAG AGTAAGTGGA CAAAATCCAA CAAGTAGTAA TAAAACAATA AATGTAATAA GAGATAAATT AGTAAAATGT GGAGGAATAA GTTTATTAGT ACAAAATACA AGTTGGTTAT TATTATTATT ATTAAGTTTA AGTTTTTTAC AAGCAACAGA TTTTATAAGT TTATGA	360 420 480 486
(2) INFORMATION FOR SEQ ID NO:37:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 485 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:	
ATGAACCCAG TCATCAGCAT CACTCTCCTG CTTTCAGTCT TGCAGATGTC CCGAGGACAG AGGGTGATCA GCCTGACAGC CTGCCTGGTG AACAGAACCT TCGACTGGAC TGCCGTCATG AGAATAACAC CAACTTGCCC ATCCAGCATG AGTTCAGCCT GACCCGAGAG AAGAAGAAGC ACGTGCTGTC AGGCACCCTG GGGGTTCCCG AGCACACTTA CCGCTCCCGC GTCAACCTTT TCAGTGACCG CTTTATCAAG GTCCTTACTC TAGCCAACTT GACCACCAAG GATGAGGGCG ACTACATGTG TGAACTTCGA GTCTCGGGCC AGAATCCCAC AAGCTCCAAT AAAACTATCA ATGTGATCAG AGACAAGCTG GTCAAGTGTG GTGGCATAAG CCTGCTGGTT CAAAACACTT CCTGGCTGCT GCTGCTCCTG CTTTCCCTCT CCTTCCTCCA AGCCACGGAC TTCATTTCTC TGTGA	60 120 180 240 300 360 420 480 485
(2) INFORMATION FOR SEQ ID NO:38:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 33 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: Other	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:	
CGCGGGGCTA GCGCAAAGAG TAATAAGTTT AAC	33
(2) INFORMATION FOR SEQ ID NO:39:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 28 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: Other	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:	
CGCGGATCCC TTGTATTTG TACTAATA	28
(2) INFORMATION FOR SEQ ID NO:40:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 762 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GAATTCACGC	GTAAGCTTGC	CGCCACCATG	GTGAGCAAGG	GCGAGGAGCT	GTTCACCGGG	60
GTGGTGCCCA	TCCTGGTCGA	GCTGGACGGC	GACGTGAACG	GCCACAAGTT	CAGCGTGTCC	120
GGCGAGGGCG	AGGGCGATGC	CACCTACGGC	AAGCTGACCC	TGAAGTTCAT	CTGCACCACC	180
GGCAAGCTGC	CCGTGCCCTG	GCCCACCCTC	GTGACCACCT	TCAGCTACGG	CGTGCAGTGC	240
TTCAGCCGCT	ACCCCGACCA	CATGAAGCAG	CACGACTTCT	TCAAGTCCGC	CATGCCCGAA	300
GGCTACGTCC	AGGAGCGCAC	CATCTTCTTC	AAGGACGACG	GCAACTACAA	GACCCGCGCC	360
GAGGTGAAGT	TCGAGGGCGA	CACCCTGGTG	AACCGCATCG	AGCTGAAGGG	CATCGACTTC	420
AAGGAGGACG	GCAACATCCT	GGGGCACAAG	CTGGAGTACA	ACTACAACAG	CCACAACGTC	480
TATATCATGG	CCGACAAGCA	GAAGAACGGC	ATCAAGGTGA	ACTTCAAGAT	CCGCCACAAC	540
ATCGAGGACG	GCAGCGTGCA	GCTCGCCGAC	CACTACCAGC	AGAACACCCC	CATCGGCGAC	600
GGCCCCGTGC	TGCTGCCCGA	CAACCACTAC	CTGAGCACCC	AGTCCGCCCT	GAGCAAAGAC	660
CCCAACGAGA	AGCGCGATCA	CATGGTCCTG	CTGGAGTTCG	TGACCGCCGC	CGGGATCACT	720
CACGGCATGG	ACGAGCTGTA	CAAGTAAAGC	GGCCGCGGAT	CC		762

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4670 base pairs(B) TYPE: nucleic acid

 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

7 7 C C C C C C T 7 7 7 C		aaamamamaa	n n aaaamaaa		OMO OMO O GO N	C 0
AAGCTTAAAC	CATGCCCATG	GGGTCTCTGC		CACCTTGTAC	CTGCTGGGGA	60
TGCTGGTCGC	TTCCGTGCTA	GCCGCCACCA	GAAGATACTA	CCTGGGTGCA	GTGGAACTGT	120
CATGGGACTA	TATGCAAAGT	GATCTCGGTG	AGCTGCCTGT	GGACGCAAGA	TTTCCTCCTA	180
GAGTGCCAAA	ATCTTTTCCA	TTCAACACCT	CAGTCGTGTA	CAAAAAGACT	CTGTTTGTAG	240
AATTCACGGA	TCACCTTTTC	AACATCGCTA	AGCCAAGGCC	ACCCTGGATG	GGTCTGCTAG	300
GTCCTACCAT	CCAGGCTGAG	GTTTATGATA	CAGTGGTCAT	TACACTTAAG	AACATGGCTT	360
CCCATCCTGT	CAGTCTTCAT	GCTGTTGGTG	TATCCTACTG	GAAAGCTTCT	GAGGGAGCTG	420
AATATGATGA	TCAGACCAGT	CAAAGGGAGA	AAGAAGATGA	TAAAGTCTTC	CCTGGTGGAA	480
GCCATACATA	TGTCTGGCAG	GTCCTGAAAG	AGAATGGTCC	AATGGCCTCT	GACCCACTGT	540
GCCTTACCTA	CTCATATCTT	TCTCATGTGG	ACCTGGTAAA	AGACTTGAAT	TCAGGCCTCA	600
TTGGAGCCCT	ACTAGTATGT	AGAGAAGGGA	GTCTGGCCAA	GGAAAAGACA	CAGACCTTGC	660
ACAAATTTAT	ACTACTTTTT	GCTGTATTTG	ATGAAGGGAA	AAGTTGGCAC	TCAGAAACAA	720
AGAACTCCTT	GATGCAGGAT	AGGGATGCTG	CATCTGCTCG	GGCCTGGCCT	AAAATGCACA	780
CAGTCAATGG	TTATGTAAAC	AGGTCTCTGC	CAGGTCTGAT	TGGATGCCAC	AGGAAATCAG	840
TCTATTGGCA	TGTGATTGGA	ATGGGCACCA	CTCCTGAAGT	GCACTCAATA	TTCCTCGAAG	900
GTCACACATT	TCTTGTGAGG	AACCATCGCC	AGGCGTCCTT	GGAAATCTCG	CCAATAACTT	960
TCCTTACTGC	TCAAACACTC	TTGATGGACC	TTGGACAGTT	TCTACTGTTT	TGTCATATCT	1020
CTTCCCACCA	ACATGATGGC	ATGGAAGCTT	ATGTCAAAGT	AGACAGCTGT	CCAGAGGAAC	1080
CCCAACTACG	AATGAAAAAT	AATGAAGAAG	CGGAAGACTA	TGATGATGAT	CTTACTGATT	1140
CTGAAATGGA	TGTGGTCAGG	TTTGATGATG	ACAACTCTCC	TTCCTTTATC	CAAATTCGCT	1200
CAGTTGCCAA	GAAGCATCCT	AAAACTTGGG	TACATTACAT	TGCTGCTGAA	GAGGAGGACT	1260
GGGACTATGC	TCCCTTAGTC	CTCGCCCCCG	ATGACAGAAG	TTATAAAAGT	CAATATTTGA	1320
ACAATGGCCC	TCAGCGGATT	GGTAGGAAGT	ACAAAAAAGT	CCGATTTATG	GCATACACAG	1380
ATGAAACCTT	TAAGACTCGT	GAAGCTATTC	AGCATGAATC	AGGAATCTTG	GGACCTTTAC	1440
TTTATGGGGA	AGTTGGAGAC	ACACTGTTGA	TTATATTTAA	GAATCAAGCA	AGCAGACCAT	1500
ATAACATCTA	CCCTCACGGA	ATCACTGATG	TCCGTCCTTT	GTATTCAAGG	AGATTACCAA	1560
AAGGTGTAAA	ACATTTGAAG	GATTTTCCAA	TTCTGCCAGG	AGAAATATTC	AAATATAAAT	1620
GGACAGTGAC	TGTAGAAGAT	GGGCCAACTA	AATCAGATCC	TCGGTGCCTG	ACCCGCTATT	1680
ACTCTAGTTT	CGTTAATATG	GAGAGAGATC	TAGCTTCAGG	ACTCATTGGC	CCTCTCCTCA	1740
TCTGCTACAA	AGAATCTGTA	GATCAAAGAG	GAAACCAGAT	AATGTCAGAC	AAGAGGAATG	1800
TCATCCTGTT	TTCTGTATTT	GATGAGAACC			AATATACAAC	1860
	CAATCCAGCT				GCCTCCAACA	1920
TCATGCACAG	CATCAATGGC	TATGTTTTTG	ATAGTTTGCA		TGTTTGCATG	1980
	CTGGTACATT	CTAAGCATTG	GAGCACAGAC		TCTGTCTTCT	2040
TCTCTGGATA			TCTATGAAGA			2100
	AACTGTCTTC	ATGTCGATGG	AAAACCCAGG			2160
	CTTTCGGAAC					2220
ACAAC I CAGA	CITICGGAAC	AGAGGCAIGA	CCGCCTIMCT	OAAGGIIICI	HOMETTON	2220

AGAACACTGG	TGATTATTAC	GAGGACAGTT	ATGAAGATAT	TTCAGCATAC	TTGCTGAGTA	2280
AAAACAATGC	CATTGAACCA	AGAAGCTTCT	CCCAGAATTC	AAGACACCCT	AGCACTAGGC	2340
AAAAGCAATT	TAATGCCACC	CCACCAGTCT	TGAAACGCCA	TCAACGGGAA	ATAACTCGTA	2400
CTACTCTTCA	GTCAGATCAA	GAGGAAATTG	ACTATGATGA	TACCATATCA	GTTGAAATGA	2460
AGAAGGAAGA	TTTTGACATT	TATGATGAGG	ATGAAAATCA	GAGCCCCCGC	AGCTTTCAAA	2520
AGAAAACACG	ACACTATTTT	ATTGCTGCAG	TGGAGAGGCT	CTGGGATTAT	GGGATGAGTA	2580
GCTCCCCACA	TGTTCTAAGA	AACAGGGCTC	AGAGTGGCAG	TGTCCCTCAG	TTCAAGAAAG	2640
TTGTTTTCCA	GGAATTTACT	GATGGCTCCT	TTACTCAGCC	CTTATACCGT	GGAGAACTAA	2700
ATGAACATTT	GGGACTCCTG	GGGCCATATA	TAAGAGCAGA	AGTTGAAGAT	AATATCATGG	2760
TAACTTTCAG	AAATCAGGCC	TCTCGTCCCT	ATTCCTTCTA	TTCTAGCCTT	ATTTCTTATG	2820
AGGAAGATCA	GAGGCAAGGA	GCAGAACCTA	GAAAAAACTT	TGTCAAGCCT	AATGAAACCA	2880
AAACTTACTT	TTGGAAAGTG	CAACATCATA	TGGCACCCAC	TAAAGATGAG	TTTGACTGCA	2940
AAGCCTGGGC	TTATTTCTCT	GATGTTGACC	TGGAAAAAGA	TGTGCACTCA	GGCCTGATTG	3000
GACCCCTTCT	GGTCTGCCAC	ACTAACACAC	TGAACCCTGC	TCATGGGAGA	CAAGTGACAG	3060
TACAGGAATT	TGCTCTGTTT	TTCACCATCT	TTGATGAGAC	CAAAAGCTGG	TACTTCACTG	3120
AAAATATGGA	AAGAAACTGC	AGGGCTCCCT	GCAATATCCA	GATGGAAGAT	CCCACTTTTA	3180
AAGAGAATTA	TCGCTTCCAT	GCAATCAATG	GCTACATAAT	GGATACACTA	CCTGGCTTAG	3240
TAATGGCTCA	GGATCAAAGG	ATTCGATGGT	ATCTGCTCAG	CATGGGCAGC	AATGAAAACA	3300
TCCATTCTAT	TCATTTCAGT	GGACATGTGT	TCACTGTACG	AAAAAAAGAG	GAGTATAAAA	3360
TGGCACTGTA	CAATCTCTAT	CCAGGTGTTT	TTGAGACAGT	GGAAATGTTA	CCATCCAAAG	3420
CTGGAATTTG	GCGGGTGGAA	TGCCTTATTG	GCGAGCATCT	ACATGCTGGG	ATGAGCACAC	3480
TTTTTCTGGT	GTACAGCAAT	AAGTGTCAGA	CTCCCCTGGG	AATGGCTTCT	GGACACATTA	3540
GAGATTTTCA	GATTACAGCT	TCAGGACAAT	ATGGACAGTG	GGCCCCAAAG	CTGGCCAGAC	3600
TTCATTATTC	CGGATCAATC	AATGCCTGGA	GCACCAAGGA	GCCCTTTTCT	TGGATCAAGG	3660
TGGATCTGTT	GGCACCAATG	ATTATTCACG	GCATCAAGAC	CCAGGGTGCC	CGTCAGAAGT	3720
TCTCCAGCCT	CTACATCTCT	CAGTTTATCA	TCATGTATAG	TCTTGATGGG	AAGAAGTGGC	3780
AGACTTATCG	AGGAAATTCC	ACTGGAACCT	TAATGGTCTT	CTTTGGCAAT	GTGGATTCAT	3840
CTGGGATAAA	ACACAATATT	TTTAACCCTC	CAATTATTGC	TCGATACATC	CGTTTGCACC	3900
CAACTCATTA	TAGCATTCGC	AGCACTCTTC	GCATGGAGTT	GATGGGCTGT	GATTTAAATA	3960
GTTGCAGCAT	GCCATTGGGA	ATGGAGAGTA	AAGCAATATC	AGATGCACAG	ATTACTGCTT	4020
CATCCTACTT	TACCAATATG	TTTGCCACCT	GGTCTCCTTC	AAAAGCTCGA	CTTCACCTCC	4080
AAGGGAGGAG	TAATGCCTGG	AGACCTCAGG	TGAATAATCC	AAAAGAGTGG	CTGCAAGTGG	4140
ACTTCCAGAA	GACAATGAAA	GTCACAGGAG	TAACTACTCA	GGGAGTAAAA	TCTCTGCTTA	4200
CCAGCATGTA	TGTGAAGGAG	TTCCTCATCT	CCAGCAGTCA	AGATGGCCAT	CAGTGGACTC	4260
TCTTTTTCA	GAATGGCAAA	GTAAAGGTTT	TTCAGGGAAA	TCAAGACTCC	TTCACACCTG	4320
TGGTGAACTC	TCTAGACCCA	CCGTTACTGA	CTCGCTACCT	TCGAATTCAC	CCCCAGAGTT	4380
GGGTGCACCA	GATTGCCCTG	AGGATGGAGG	TTCTGGGCTG	CGAGGCACAG	GACCTCTACT	4440
GAGGGTGGCC	ACTGCAGCAC	CTGCCACTGC	CGTCACCTCT	CCCTCCTCAG	CTCCAGGGCA	4500
GTGTCCCTCC	CTGGCTTGCC	TTCTACCTTT	GTGCTAAATC	CTAGCAGACA	CTGCCTTGAA	4560
GCCTCCTGAA	TTAACTATCA	TCAGTCCTGC	ATTTCTTTGG	TGGGGGGCCA	GGAGGGTGCA	4620
TCCAATTTAA	CTTAACTCTT	ACCGTCGACC	TGCAGGCCCA	ACGCGGCCGC		4670

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

AAGCTTAAAC	CATGCCCATG	GGGTCTCTGC	AACCGCTGGC	CACCTTGTAC	CTGCTGGGGA	60
TGCTGGTCGC	TTCCGTGCTA	GCCGCCACCC	GCCGCTACTA	CCTGGGCGCC	GTGGAGCTGT	120
CCTGGGACTA	CATGCAGAGC	GACCTGGGCG	AGCTCCCCGT	GGACGCCCGC	TTCCCCCCCC	180
GCGTGCCCAA	GAGCTTCCCC	TTCAACACCA	GCGTGGTGTA	CAAGAAAACC	CTGTTCGTGG	240
AGTTCACCGA	CCACCTGTTC	AACATTGCCA	AGCCGCGCCC	CCCCTGGATG	GGCCTGCTGG	300
GCCCCACCAT	CCAGGCCGAG	GTGTACGACA	CCGTGGTGAT	CACCCTGAAG	AACATGGCCA	360
GCCACCCCGT	CAGCCTGCAC	GCCGTGGGCG	TGAGCTACTG	GAAGGCCAGC	GAGGGCGCCG	420
AGTACGACGA	CCAGACGTCC	CAGCGCGAGA	AGGAGGACGA	CAAGGTGTTC	CCGGGGGGGA	480
GCCACACCTA	CGTGTGGCAG	GTGCTTAAGG	AGAACGGCCC	TATGGCCAGC	GACCCCCTGT	540
GCCTGACCTA	CAGCTACCTG	AGCCACGTGG	ACCTGGTGAA	GGATCTGAAC	AGCGGGCTGA	600
TCGGCGCCCT	GCTGGTGTGT	CGCGAGGGCA	GCCTGGCCAA	GGAGAAAACC	CAGACCCTGC	660

ACAAGTTCAT	CCTGCTGTTC	GCCGTGTTCG	ACGAGGGGAA	GAGCTGGCAC	AGCGAGACTA	720
AGAACAGCCT	GATGCAGGAC	CGCGACGCCG	CCAGCGCCCG	CGCCTGGCCC	AAGATGCACA	780
CCGTTAACGG	CTACGTGAAC	CGCAGCCTGC	CCGGCCTGAT	CGGCTGCCAC	CGCAAGAGCG	840
TGTACTGGCA	CGTCATCGGC	ATGGGCACCA	CCCCTGAGGT	GCACAGCATC	TTCCTGGAGG	900
GCCACACCTT	CCTGGTGCGC	AACCACCGCC	AGGCCAGCCT	GGAGATCAGC	CCCATCACCT	960
TCCTGACTGC	CCAGACCCTG	CTGATGGACC	TAGGCCAGTT	CCTGCTGTTC	TGCCACATCA	1020
GCAGCCACCA		ATGGAGGCTT	ACGTGAAGGT	GGACAGCTGC	CCCGAGGAGC	1020
CCCAGCTGCG	CATGAAGAAC		CCGAGGACTA	CGACGACGAC		
			-	-	CTGACCGACA	1140
GCGAGATGGA	TGTCGTACGC	TTCGACGACG	ACAACAGCCC	CAGCTTCATC	CAGATCCGCA	1200
GCGTGGCCAA	GAAGCACCCT	AAGACCTGGG	TGCACTACAT	CGCCGCCGAG	GAGGAGGACT	1260
GGGACTACGC	CCCGCTAGTA		ACGACCGCAG	CTACAAGAGC	CAGTACCTGA	1320
ACAACGGCCC	CCAGCGCATC	GGCCGCAAGT		GCGCTTCATG	GCCTACACCG	1380
ACGAGACTTT	CAAGACCCGC	GAGGCCATCC	AGCACGAGTC	CGGCATCCTC	GGCCCCCTGC	1440
TGTACGGCGA	GGTGGGCGAC	ACCCTGCTGA	TCATCTTCAA	GAACCAGGCC	AGCAGGCCCT	1500
ACAACATCTA	CCCCCACGGC	ATCACCGACG	TGCGCCCCCT	GTACAGCCGC	CGCCTGCCCA	1560
AGGGCGTGAA	GCACCTGAAG	GACTTCCCCA	TCCTGCCCGG	CGAGATCTTC	AAGTACAAGT	1620
GGACCGTGAC	CGTGGAGGAC	GGCCCCACCA	AGAGCGACCC	CCGCTGCCTG	ACCCGCTACT	1680
ACAGCAGCTT	CGTGAACATG	GAGCGCGACC	TGGCCTCCGG	ACTGATCGGC	CCCCTGCTGA	1740
TCTGCTACAA	GGAGAGCGTG	GACCAGCGCG	GCAACCAGAT	CATGAGCGAC	AAGCGCAACG	1800
TGATCCTGTT	CAGCGTGTTC	GACGAGAACC	GCAGCTGGTA	TCTGACCGAG	AACATCCAGC	1860
GCTTCCTGCC	CAACCCCGCT	GGCGTGCAGC	TGGAAGATCC	CGAGTTCCAG	GCCAGCAACA	1920
	CATCAACGGC		ACAGCCTGCA		TGCCTGCATG	1980
AGGTGGCCTA	CTGGTACATC	CTGAGCATCG	GCGCCCAGAC		AGCGTGTTCT	2040
TCTCCGGGTA	TACCTTCAAG	CACAAGATGG	TGTACGAGGA		CTGTTCCCCT	
						2100
TCTCCGGCGA	GACTGTGTTC		AGAACCCCGG	CCTGTGGATT	CTGGGCTGCC	2160
ACAACAGCGA	CTTCCGCAAC	CGCGGCATGA		GAAAGTCTCC	AGCTGCGACA	2220
AGAACACCGG	CGACTACTAC	GAGGACAGCT		CTCCGCCTAC	CTGCTGTCCA	2280
AGAACAACGC	CATCGAGCCC	CGCTCCTTCT	CCCAAAACTC	CCGCCACCCC	AGCACGCGTC	2340
AGAAGCAGTT	CAACGCCACC	CCCCCCGTGC	TGAAGCGCCA	CCAGCGCGAG	ATCACCCGCA	2400
CCACCCTGCA	AAGCGACCAG	GAGGAGATCG	ACTACGACGA	CACCATCAGC	GTGGAGATGA	2460
AGAAGGAGGA	CTTCGACATC	TACGACGAGG	ACGAGAACCA	GAGCCCCCGC	TCCTTCCAAA	2520
AGAAAACCCG	CCACTACTTC	ATCGCCGCCG.	TGGAGCGCCT	GTGGGACTAC	GGCATGAGCA	2580
GCAGCCCCCA	CGTCCTGCGC	AACCGCGCCC	AGAGCGGCAG	CGTGCCCCAG	TTCAAGAAGG	2640
TGGTGTTCCA	GGAGTTCACC	GACGGCAGCT	TCACCCAGCC	CCTGTACCGC	GGCGAGCTGA	2700
ACGAGCACCT	GGGCCTGCTC	GGCCCCTACA	TCCGCGCCGA	GGTGGAGGAC	AACATCATGG	2760
TGACCTTCCG	CAACCAAGCC		ACTCCTTCTA		ATCAGCTACG	2820
AGGAGGACCA	GCGCCAGGGC	GCCGAGCCCC		CGTGAAGCCC	AACGAGACTA	2880
AGACCTACTT	CTGGAAGGTG	CAGCACCACA		CAAGGACGAG	TTCGACTGCA	2940
AGGCCTGGGC	CTACTTCAGC	GACGTGGACC			GGCCTGATCG	3000
GCCCCCTGCT	GGTGTGCCAC	ACCAACACCC	TGAACCCCCC	CCACGGGAGG	CAGGTGACTG	3060
TGCAGGAATT	TGCCCTGTTC	TTCACCATCT	TCGACGAGAC	TAAGAGCTGG	TACTTCACCG	3120
AGAACATGGA	GCGCAACTGC	CGCGCCCCT		GATGGAAGAT	CCCACCTTCA	3180
AGGAGAACTA	CCGCTTCCAC	GCCATCAACG	GCTACATCAT	GGACACCCTG	CCCGGCCTGG	3240
TGATGGCCCA		ATCCGCTGGT		TATGGGCAGC		3300
TCCACAGCAT	CCACTTCAGC	GGCCACGTTT	TCACCGTGCG	CAAGAAGGAG	GAGTACAAGA	3360
TGGCCCTGTA	CAACCTGTAC	CCCGGCGTGT	TCGAGACTGT	GGAGATGCTG	CCCAGCAAGG	3420
CCGGGATCTG	GCGCGTGGAG	TGCCTGATCG	GCGAGCACCT	GCACGCCGGC	ATGAGCACCC	3480
TGTTCCTGGT	GTACAGCAAC	AAGTGCCAGA	CCCCCTGGG	CATGGCCAGC	GGCCACATCC	3540
GCGACTTCCA	GATCACCGCC	AGCGGCCAGT	ACGGCCAGTG	GGCTCCCAAG	CTGGCCCGCC	3600
TGCACTACAG	CGGCAGCATC	AACGCCTGGT	CGACCAAGGA	GCCCTTCTCC	TGGATCAAGG	3660
TGGACCTGCT	GGCCCCCATG	ATCATCCACG	GCATCAAGAC	CCAGGGCGCC	CGCCAGAAGT	3720
TCAGCAGCCT	GTACATCAGC	CAGTTCATCA	TCATGTACTC	TCTAGACGGC	AAGAAGTGGC	3780
AGACCTACCG	CGGCAACAGC	ACCGGCACCC	TGATGGTGTT	CTTCGGCAAC	GTGGACAGCA	3840
GCGGCATCAA	GCACAACATC	TTCAACCCCC	CCATCATCGC	CCGCTACATC	CGCCTGCACC	3900
CCACCCACTA	CAGCATCCGC	AGCACCCTGC		GATGGGCTGC	GACCTGAACA	3960
GCTGCAGCAT	GCCCCTGGGC	ATGGAGAGCA		CGACGCCCAG	ATCACCGCCT	4020
CCAGCTACTT	CACCAACATG	TTCGCCACCT	GGAGCCCCAG	CAAGGCCCGC	CTGCACCTGC	
						4080
AGGGCCGCAG	CAACGCCTGG	CGCCCCCAGG	TGAACAACCC	CAAGGAGTGG	CTGCAGGTGG	4140
ACTTCCAGAA	AACCATGAAG	GTGACTGGCG	TGACCACCCA	GGGCGTCAAG	AGCCTGCTGA	4200
CCAGCATGTA	CGTGAAGGAG	TTCCTGATCA	GCAGCAGCCA	GGACGGCCAC	CAGTGGACCC	4260
TGTTCTTCCA	AAACGGCAAG	GTGAAGGTGT	TCCAGGGCAA	CCAGGACAGC	TTCACACCGG	4320
TCGTGAACAG	CCTGGACCCC	CCCCTGCTGA	CCCGCTACCT	GCGCATCCAC	CCCCAGAGCT	4380
GGGTGCACCA	GATCGCCCTG	CGCATGGAGG	TGCTGGGCTG	CGAGGCCCAG	GACCTGTACT	4440
GAAGCGGCCG	C					4451

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	(2) INFORMATION FOR SEQ ID NO:43:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: Other	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:	
GGGGATC	CTC ACGTCTCA	18
	(2) INFORMATION FOR SEQ ID NO:44:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 33 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: Other	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:	
CTGCTTC	TGA CGCGTGCTGG GGTGGCGGGA GTT	33
	(2) INFORMATION FOR SEQ ID NO:45:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: Other	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:	
CTGCTGA	AAG TCTCCAGCTG C	21
	(2) INFORMATION FOR SEQ ID NO:46:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 33 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: Other	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:	
GGCAGGT	GCT TAAGGAGAAC GGCCCTATGG CCA	33
	(2) INFORMATION FOR SEQ ID NO:47:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: Other	